

Corrigendum

Corrigendum to Horner, P. and Adams, M. (2007). A molecular systematic assessment of species boundaries in Australian *Cryptoblepharus* (Reptilia: Squamata: Scincidae) – a case study for the combined use of allozymes and morphology to explore cryptic biodiversity. *The Beagle, Records of the Museums and Art Galleries of the Northern Territory, Supplement 3*: 1-19.

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In the published version of this article three tables, referred to in this text as Tables 1, 2 and 3 were omitted in error. This error does not change the conclusions of the study in any way and the authors wish to apologise for the omission. The paper should have contained the three following tables.

Table 1. Allozyme frequencies for the 11 diagnosable OTUs identified within lineage 1, plus the two extralimital species. For polymorphic loci, the frequencies of all but the rarer/rarest alleles are expressed as percentages and shown as superscripts (allowing the frequency of each rare allele to be calculated by subtraction from 100%). Alleles not separated by a comma all shared the frequency indicated. The following loci were invariant: *Gapd³*, *Lap¹*, *Pgam¹*, and *Sod¹*.

Locus	carn D	mega A1	mega A2	mega A3	mega A4	plag A1	plag A2	plag A3	plag A4	plag A5	plag B	egcr	novo	
Acon-1	b	b	b	b	b	b	b	b	b	b ⁹⁹ ,a	b	b	e ⁵⁰ ,c ²⁵ ,b	
Acon-2	c ⁷⁷ ,d ¹⁵ ,b	c	c ⁶⁰ ,d ¹⁵ ,f	b	c	c ⁹³ ,d	c	c ⁸³ ,d	c ⁷³ ,g	c ⁵⁴ ,d ¹⁹ ,f ⁸ ,b ³ ,g	c ⁶⁴ ,b ²⁸ ,d ⁵ ,a ³ ,g	d	f	
Acp	c	c	c	c	c	c ⁹⁷ ,c	c	c	c ⁹⁷ ,a ³	c ⁹⁹ ,f	c ⁹⁷ ,f ² ,b	c	d	
Acyc	c	c	c	c	c	c	c	c	c ⁹⁷ ,e	c ⁹⁸ ,bd ¹	c ⁹⁶ ,e	c	a	
Ada	o ⁸⁸ ,n ⁷ ,l ³ ,p	q ⁶⁷ ,o ³³	i ⁵⁵ ,c ⁴⁰ ,f	i	f ⁸⁸ ,l	c ⁹¹ ,f ⁶ ,b	f	f	f ⁹⁸ ,f ²	o ⁸⁵ ,n ²¹ ,l ¹ ,m ³ ,kip ² ,hgrs ¹	c ⁶⁶ ,f ³² ,el ¹	d	a	
Adh-1	b ⁹⁷ ,a ² ,c	b	b	b	b	b	b	b	b	b	b	b	a	
Adh-2	e ⁸⁸ ,bc ⁵ ,f	e	e ⁹⁵ ,f	e	e	e ⁹⁷ ,h	e	e	e ⁹³ ,h	e ⁸² ,c ⁴ ,f ² ,ag ¹	e ⁸⁴ ,g ² ,a	h	c	
Alb	c	c	c	c	c ⁶³ ,d	c	c	c	d	c ⁹⁸ ,ab ¹	c ⁹⁹ ,b	b ⁵⁰ ,c	b	
Ca	b	b	b	b	b	b	b	b	b ⁹⁷ ,a	b	b	b	b	
Cs	b	b	b	b	b	b	b	b	b	b	b	a	b	
Dia	h ⁹⁶ ,j	b	b ⁶⁵ ,d	i	d ⁸⁸ ,g	b ⁶⁴ ,d	f ⁹⁰ ,d ³³ ,b	d ³³ ,j	d ⁹⁵ ,g ³ ,h	h ⁸⁵ ,j	e ⁸¹ ,h ¹⁸ ,k	h	j	
Enol	b	b	b	b	b	b	b	b	b ⁹⁷ ,a	b ⁹⁹ ,c	b ⁹⁹ ,c	b	e	
Fdp	b	b	b	b	b	b ⁸⁸ ,d ¹²	b	b ⁸³ ,d ¹⁷	b	b ⁹⁹ ,a	b	b	c	
Fum	h ⁹⁰ ,j	h	h	h	h	h ⁹¹ ,d	h	h	h ⁷² ,d	h ⁸² ,d ¹³ ,j ² ,ail ¹	h ⁹⁷ ,j ² ,f	k	h ⁷⁵ ,d	
Gda	e ⁸⁵ ,g ¹³ ,h	c	c ⁷⁰ ,e	e	e	c ⁸⁸ ,e ¹²	e ⁸³ ,g	c	c ⁹⁷ ,c	c ⁹⁶ ,g	c ⁹⁵ ,a	c	c	
Gdh	a	a	a	a	a	a	a	a	a	a	a	a	b	
Glo	d	d	d	d	b ⁵⁰ ,d ⁵⁰	d	d	d	d	d ⁹⁹ ,c	d ⁹⁹ ,a	d	d	
Got-1	b	b	b ⁹⁵ ,d	b	b	b ⁹⁷ ,a	b	b	b	b	b ⁹⁴ ,d ³ ,c ² ,a	b	b	
Got-2	i ⁹⁵ ,k ³ ,e	m	m ⁹⁵ ,l	i	f	g ⁷⁵ ,f	f ⁸³ ,g	f ⁹⁷ ,g	f ⁹³ ,h ¹ ,gi ²	i ⁹⁸ ,ek ¹	i ⁹⁹ ,k	c	a	
Gpd	e ⁹⁸ ,b	c	c	c	c	c	c	c	c	c ⁹⁸ ,ab ¹	c ⁹⁹ ,b	c	c ⁷⁵ ,d	
Gpi	a ⁹³ ,c ⁴ ,f	f ⁹⁷ ,i	f ⁹⁰ ,a	a	f ⁷⁵ ,i	f ⁹¹ ,a	f	f	f	a ⁹⁸ ,f ² ,g ¹	d ⁹⁷ ,j ² ,i	a	h	
Gpx	e ⁹⁸ ,a	e	e	e	e	e	e	e	e ⁹⁵ ,c	e ⁹⁹ ,c	e ⁹⁸ ,cd ¹	e	e	
Guk	e ⁹⁷ ,f	a ⁶⁷ ,b	f	i	f ⁵⁷ ,e	f ⁸⁴ ,e	f	f	f	c ⁷⁵ ,f ¹² ,e ⁸ ,d ³ ,gh ¹	b ⁸² ,d ¹¹ ,c ⁶ ,a	h	g	
Hbdh	e ⁵² ,k ²⁹ ,j ⁷ ,m ⁷ ,c ³ ,h	h ⁶⁷ ,j	j ⁹⁵ ,l	e	g ⁶³ ,c ²⁵ ,j	g ⁶⁶ ,j ²⁸ ,bc ³	d ³³ ,g ³³ ,c ¹² ,j	b ⁵⁰ ,c ²⁵ ,g	c ⁶⁵ ,g ²⁸ ,a ¹⁵ ,b ¹⁰ ,h	g ⁷¹ ,m ⁸ ,h ⁷ ,j ⁶ ,ko ² ,ccf ¹	i ⁹¹ ,j ⁶ ,h	j	d	
Idh	e ⁹⁷ ,a ² ,d	c	c	c	c ⁵⁰ ,f	f ⁹⁷ ,c	f ⁸³ ,c	f	f ⁹⁸ ,i	c ⁹⁴ ,d ⁴ ,ef ¹	c ⁸⁶ ,f ¹² ,be ¹	h	g	
Ldh	a	a	a	a	a	a	a	a	a	a	a	b	a	
Mdh-1	b	b	b	b	b	b	b	b	b	b	b ⁹⁷ ,a	b	b	
Mdh-2	a	a	a	a	a	a	a	a	a	a ⁹⁹ ,c	a	a	b	
Mpi	e ⁹⁸ ,f	c	c	a	c	c	c	c	c ⁹⁰ ,h ³³ ,f	c ⁸⁸ ,f	c ⁹⁸ ,bc ¹	c ⁷⁸ ,f ¹⁷ ,d ³ ,eg ¹	f	g
Np	b	b	b	b	b	b	b	b	b	b ⁹⁹ ,a	b	b	d	
PepA-1	e ⁹⁸ ,f	e	e ⁶⁵ ,h	e	e	e	e	e	e	e ⁹⁹ ,d	e ⁸⁷ ,g	e	g	
PepA-2	d ⁹² ,e ⁶ ,c	c	d ⁹⁰ ,c	g	d	d	d	d	d	e ⁹⁹ ,d ²⁹ ,bf ¹	d ⁹³ ,e ⁶ ,e	d	e ⁵⁰ ,g	
PepB	d ⁹⁸ ,a ²	g	g ⁵⁵ ,i ⁴⁵	g	b ⁵⁰ ,d ⁵⁰	d ⁹¹ ,b ² ,g ¹ ,h ¹	d ⁸³ ,g ¹⁷	d	d ⁸⁵ ,e ¹³ ,g ²	d ⁸⁷ ,g ⁷ ,ch ² ,ab ¹	g ⁹³ ,h ⁴ ,d	d	d	
PepD-1	b ⁹⁰ ,a ¹⁵ ,d ¹ ,e	h	d	b	b	b	b	b	b ⁹⁸ ,d	b ⁹⁸ ,d ³ ,a	d ⁶⁷ ,e ³² ,a	a ⁸⁰ ,d	i	
PepD-2	d ⁹⁵ ,g ² ,b	c	b ⁹⁰ ,e	g	d ⁶² ,b	e ⁶⁶ ,h ²⁸ ,dj ³	b ⁶⁷ ,d ¹⁷ ,f	d ⁶⁷ ,b ¹⁷ ,e	d ⁹² ,g ⁵ ,b	d ⁸⁷ ,b ¹ ,a ³ ,egh ¹	d ⁹⁶ ,a	b	a	
6Pgd	f ³³ ,e ⁷ ,hi ¹ ,bk ²	f	f ⁹⁸ ,h	d ⁹⁰ ,g	f	f ⁹¹ ,d ⁶ ,i	f	f	f ⁹⁰ ,i	f ⁹⁴ ,bd ³ ,el ¹	f	f	d ⁷⁵ ,f	
Pgk	b ⁹⁸ ,c	c ⁵⁰ ,f	e ⁹⁰ ,c	c	c	el ¹	c	c	c ⁹⁷ ,b	b ⁹¹ ,c ⁶ ,d	c	c	c	
Pgm-1	c ⁸⁶ ,e ⁷ ,h ³ ,f	d	d ⁷⁰ ,c	a ⁶³ ,c ²⁵ ,f	c ⁷³ ,f	c ⁵⁰ ,f	c ⁶⁷ ,f	e ⁷⁵ ,c	c ⁹⁸ ,f	e ⁶⁷ ,e ²⁸ ,f ² ,a	e ⁹³ ,d ⁴ ,h	c	f	
Pgm-2	c ⁶⁵ ,b ³⁰ ,a ³ ,d	b	b	c	c	c ⁵⁶ ,b	c	b ⁸³ ,c	b ⁵⁵ ,a	b ⁷⁵ ,c ²⁴ ,a	b ⁹⁹ ,e	b	c	
Srdh	d	d ⁹³ ,c	d	d	d	d ⁹⁷ ,g	d	d	d ⁹⁶ ,e	d ⁹⁹ ,e	d ⁹⁵ ,g	f	f	
Tpi	b	b ⁸³ ,e	e	a	b	b	b	b	b ⁹⁵ ,a	b	f	a	d	

Table 2. Allozyme frequencies for the 16 diagnosable OTUs identified within lineage 2, plus the putative ‘virgA1x3’ hybrid population. Format as per Table 1. The following loci were invariant: *Acp-1^a*, *Alb^a*, *Gapd^a*, *Gdh^a*, *Lap^a*, *Ldh^a*, *Mdh-1^b*, *Mdh-2^a*, *Pgam^a*, *Pgk^a*, and *Sod^a*.

Locus	earn A1	earn A2	earn A3	earn A4	earn A5	earn B	earn C	fuhn	horn	litor	mega A5	mega B	virg A1	virg A2	virg A3	‘virg A1x3’	virg B	
Acon-1	d	d	d	d	d ⁸⁸ ,e	d	d	d	d	d	d ⁸³ ,a	d	d ⁷⁷ ,b	b ⁹⁴ ,d	d	d	d	
Acon-2	d ⁹⁴ ,c ⁷	d	d ⁹³ ,f	d ⁹⁰ ,c	d ⁸⁵ ,f	d	d ⁹² ,c	e	c ⁷⁰ ,d	c ⁵⁵ ,d	d	d ⁹⁰ ,g ⁷ , e	d ⁹⁰ ,c ⁶ , f	d ⁸⁷ ,c ³¹ , bc ⁶	d ⁸⁶ ,c ⁷ , g	d ⁷⁹ ,b ¹⁴ , e	d	
Acyc	c	c	c	c ⁹⁰ ,b	c	c	c	c	c	c ⁹⁵ ,d	c	c	b	c ⁹⁴ ,b	c	b ⁹⁰ ,c	b	
Ada	p	p	p	p	o ⁸⁴ ,p ⁷ , s ⁴ ,r ¹² , t	l ⁵⁹ ,i	l ⁹² ,o	j ⁷⁵ ,o	o ⁶⁰ ,j	o ⁵⁵ ,j	o	p	o ⁴⁰ ,i ²⁷ , p ¹² ,l ⁸ , js ² ,hr ² ,q	o ⁹⁴ ,s	o ⁶⁴ ,i ¹² , p	o ⁵⁷ ,i	o ⁴⁶ ,l ²⁹ , i ¹³ ,j	
Adh-1	b	b	b	b	b ⁹⁸ ,d	b	b	b	b	b	b	b	b ⁹⁸ ,a	b	b	b	b	
Adh-2	f ⁸⁸ ,d ⁶ , ij ³	f	f ⁹³ ,j	f ⁹⁰ ,e	f ⁹³ ,k ³ ,i	f	f	f	f	f	f	f	f ⁹⁷ ,i	f	f ⁹¹ ,c	f ⁸² ,ci ⁹	f ⁹⁶ ,i	f ⁷⁷ ,i
Ca	e	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	
Cs	b	b	b	b	b	b	b ⁹³ ,a	b	b	b	b	b	b	b	b	b	b	
Dia	a	h	h	h	h	h	h	d ⁹⁰ ,h	h	h	h	h	h	e ⁸¹ ,h	h	h	h	
Enol	b ⁹¹ ,d	b	b	b	b ⁹⁵ ,d	b	b	b	b	b	b	b	b	b	b	b	b	
Fdp	b	b ⁹⁰ ,d	b	b	b ⁹⁵ ,d	b	b	b	b	b	b	b	b	b	b	b	b	
Fum	e ⁹⁷ ,b	e ⁹⁰ ,b	e	e	e ⁹⁵ ,g	e ⁹⁷ ,g	e	e	e	e	e ⁹³ ,c	e ⁹⁷ ,c	e ⁹⁶ ,c	e ⁸⁴ ,j	c ⁵⁵ ,e	e ⁹⁶ ,e	e	
Gda	e	e ⁹⁰ ,h	e	e	e ⁹⁰ ,g ⁷ , bc ²	c	c ⁹⁶ ,e	e	d ⁸⁸ ,f	f		c	e ⁹² ,d ⁴ ,f	e	e	e ⁹⁰ ,f	e	
Glo	d	d	d	d	d ⁸¹ ,a	d	d	d	d	d ⁷⁵ ,a	d	d	d ⁸⁸ ,a	d	a ⁶⁴ ,d	d ⁸⁶ ,ac ⁷	d	
Got-1	b ⁹⁴ ,c	b	b	b ⁹⁰ ,c	b ⁹⁵ ,d	b	b	b	b	b	b ⁶⁷ ,c ¹⁷ ,d	b	b ⁹⁶ ,ad ²	b ⁶⁴ ,a	b	b ⁹³ ,d	b	
Got-2	d ⁹⁴ ,h	k	d	d	g ⁸¹ ,h ³⁶ ,i	d	i	d	d	d	d	d	d	d ⁸⁴ ,b	i ⁸⁶ ,g	g ⁷¹ ,i ²² ,d	g ⁹⁶ ,j	
Gpd	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	
Gpi	a	a	a	f	a ⁹⁶ ,h ¹	a	a	a	a	a	f ⁸³ ,a	a ⁹¹ ,c ⁶ ,h	a ⁹⁶ ,bg ²	a	a ⁹¹ ,d ⁵ ,g	a	a	
Gpx	e	e	e	e ⁹⁰ ,b	e	c	e	e	e	e	e ⁹⁰ ,f	e	e	e	e	e ⁹⁰ ,b	e	
Guk	e ⁹⁷ ,h	h ⁶⁰ ,e	e	e	e	e	e	e	e	e	e	e	e	e	e	e	e	
Hbdh	h ⁹⁷ ,d	m ⁸⁰ ,h	h ⁶⁴ ,d	h ⁹⁰ ,i	j ⁹⁶ ,h ³³ , k ¹⁵ ,p ⁴ ,q	h	i ⁹⁶ ,h	p ⁷⁵ ,m	m	m ⁹⁰ ,h	j	m ⁹⁴ ,dh ³	m ⁵² ,o ⁴⁶ , n	o ⁸¹ ,m ¹³ ,p	j ⁵⁰ ,h ³² , o ⁶ ,k ⁴ ,m	o ⁹⁰ ,j ²⁹ ,m	m ⁶⁹ ,o	
Idh	c	c	c ⁹³ ,h	c	c ⁸⁸ ,a	c	c	c	c	c	c	c	c	c	c	c	c	
Mpi	c	c	c ⁹³ ,f	c ⁹⁰ ,b	c ⁸⁶ ,f	c	c	c	f	f	c	c ⁸¹ ,f ¹⁶ ,b	c	c	c	c ⁹⁰ ,f	c ⁹² ,f	
Np	c	c	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b	
PepA-1	b ⁹¹ ,e	c ⁹⁰ ,a	b	e ⁹⁰ ,b ⁴⁰ ,d	e ⁸⁸ ,d	e ⁹¹ ,g	c	b	e ⁹⁰ ,f	e	e	e ⁹⁶ ,b	e ⁹⁶ ,b	e ⁸⁷ ,b	e ⁹¹ ,b	e ⁷⁹ ,b	c ⁹⁶ ,d	
PepA-2	e	e ⁶⁰ ,f	e	e	e ⁹³ ,c ⁴ ,d	e	e	b	e ⁸⁰ ,d ¹⁰ ,c	d ⁵⁰ ,e	e ⁹⁰ ,f	e ⁹⁷ ,c	b ⁹¹ ,c ¹³ , a ⁴ ,d	b ⁷⁵ ,a	e ⁵⁵ ,f ²² , d ¹⁸ ,c	d ⁵⁸ ,c ²¹ , e ¹⁴ ,b	b	
PepB	d	g ⁹⁰ ,i	h	g ⁷⁰ ,e	g ⁷⁹ ,h ¹⁵ , d ^{fi} 2	g ⁹⁴ ,d	g	g ⁷⁵ ,b	g ⁸⁰ ,d	d ⁸⁵ ,g	g	h ⁸⁸ ,d ^{fi} k ³ , g ⁷¹ ,h ²⁷ ,f	g ⁷⁵ ,h	g	g ⁶⁴ ,h ²⁹ ,d	g ⁹⁶ ,h		
PepD-1	d ⁹⁷ ,e	d ⁶⁰ ,f ³⁰ ,h	d	d	d ⁹⁶ ,bc ²	d	d ⁷⁹ ,g	h	d	d	d	d ⁸⁴ ,g	d ⁹⁸ ,e	c ⁴⁴ ,g ¹ ,d	d ⁹⁵ ,e	d ⁹³ ,e	d	
PepD-2	d ⁷⁹ ,g	d ⁹⁰ ,e	d	d	d	d ⁸⁴ ,i	d	d	d	d	d	d ⁹⁷ ,a	d	d ⁶⁰ ,e	d ⁹⁵ ,g	d	d	
6Pgd	f ⁷⁷ ,d ²⁰ ,i	f ⁷⁰ ,bd ^g 10	f ⁶⁴ ,i	f	f ⁹⁶ ,d ¹⁷ , b ⁷ ,g ¹ ,i	f	f	d	f	f	f ⁸³ ,i	f ⁹⁰ ,i ⁷ ,j	d ⁹⁴ ,ac ¹²	f ⁸⁷ ,d	d ⁷⁰ ,f	d ⁸⁰ ,f	d	
Pgm-1	d	d	d ⁷⁹ ,g	d	d ⁴³ ,a ⁴¹ , g ⁷ ,e	g	d ⁹⁶ ,g	g	c ⁹⁰ ,d	c ⁷⁵ ,a ²⁰ ,g	d ⁶⁷ ,c	d ⁹³ ,b	d ⁹⁰ ,g	d ⁸¹ ,c ¹³ ,g	d ⁸⁹ ,g ¹⁵ ,a	d ⁷⁹ ,a ¹⁴ ,g	d ⁹² ,g	
Pgm-2	c	c	e	c	c ⁸⁸ ,d	c ⁹⁷ ,b	c ⁹⁶ ,e	c	c	c	c	c	c ⁸⁸ ,e	c ⁸⁷ ,d	c	c ⁹⁵ ,d	c ⁸⁶ ,d	c
Srdh	c ⁹⁷ ,f	c	c	c	c	c	c	c	c	c	c	c	c	c ⁹⁶ ,b	c ⁹⁴ ,a	c ⁹⁰ ,b	c	c ⁷⁷ ,b
Tpi	a	a	a	a	a	a ²² ,b ²⁵ ,d	a ⁹⁶ ,b	a	b	b	a	a	a	a	a	a ⁹³ ,c	a	

Table 3. Pairwise genetic distance measures among all final OTUs. OTUs are grouped and delineated according their membership of either lineage 1 (top), lineage 2 (middle) or extralimital taxa (bottom). Lower triangle = %FD; upper triangle = Nei D.

OTU	carD	megaA1	megaA2	megaA3	megaA4	megaA5	plagA1	plagA2	plagA3	plagA4	plagA5	plagB	carA1	carA2	carA3	carA4	carA5	carB	carC	fuln	horn	litor	megaA5	megaB	virgA1	virgA2	virgA3	virgB	eger	novo	
carD	-	0.29	0.27	0.31	0.17	0.21	0.17	0.21	0.23	0.02	0.22	0.22	0.63	0.63	0.55	0.57	0.47	0.53	0.50	0.49	0.61	0.51	0.42	0.35	0.44	0.46	0.46	0.36	0.38	0.48	1.04
megaA1	27	-	0.16	0.39	0.29	0.23	0.27	0.26	0.35	0.28	0.23	0.23	0.63	0.55	0.52	0.49	0.49	0.49	0.49	0.49	0.62	0.56	0.53	0.45	0.51	0.54	0.44	0.47	0.56	0.46	1.06
megaA2	22	9	-	0.38	0.24	0.20	0.22	0.22	0.29	0.26	0.23	0.23	0.65	0.55	0.62	0.51	0.54	0.51	0.54	0.49	0.62	0.56	0.53	0.45	0.51	0.54	0.44	0.47	0.56	0.46	1.09
megaA3	27	34	27	-	0.35	0.37	0.34	0.38	0.43	0.30	0.33	0.33	0.65	0.55	0.62	0.61	0.51	0.54	0.51	0.49	0.62	0.56	0.53	0.45	0.51	0.54	0.44	0.47	0.56	0.46	0.98
megaA4	13	24	13	30	-	0.11	0.02	0.08	0.05	0.18	0.29	0.18	0.61	0.58	0.64	0.57	0.54	0.57	0.58	0.59	0.55	0.48	0.53	0.60	0.60	0.60	0.45	0.53	0.62	0.50	0.99
plagA1	16	20	11	32	7	-	0.07	0.07	0.14	0.21	0.27	0.19	0.67	0.65	0.63	0.57	0.58	0.57	0.58	0.59	0.52	0.56	0.59	0.64	0.64	0.64	0.51	0.60	0.65	0.50	0.90
plagA2	13	20	11	27	0	4	-	0.06	0.07	0.19	0.29	0.19	0.61	0.59	0.65	0.57	0.55	0.58	0.59	0.62	0.56	0.49	0.53	0.61	0.61	0.46	0.55	0.62	0.47	0.92	
plagA3	18	24	16	32	2	4	2	-	0.07	0.21	0.22	0.22	0.69	0.67	0.64	0.57	0.62	0.58	0.59	0.71	0.60	0.51	0.59	0.60	0.68	0.55	0.64	0.70	0.49	0.93	
plagA4	18	29	20	36	2	9	4	4	-	0.22	0.32	0.32	0.70	0.68	0.73	0.66	0.64	0.66	0.67	0.69	0.61	0.54	0.61	0.68	0.69	0.55	0.64	0.71	0.47	1.04	
plagA5	0	24	20	27	9	13	11	16	16	-	0.23	0.48	0.48	0.43	0.48	0.49	0.38	0.42	0.39	0.51	0.41	0.36	0.43	0.44	0.46	0.36	0.37	0.47	0.42	1.03	
plagB	18	20	18	30	27	24	24	20	27	16	-	0.65	0.56	0.56	0.50	0.50	0.48	0.45	0.45	0.62	0.54	0.51	0.47	0.52	0.56	0.45	0.46	0.58	0.53	1.01	
carA1	40	47	42	45	42	44	44	47	51	38	49	-	0.15	0.10	0.13	0.15	0.15	0.16	0.19	0.22	0.26	0.23	0.19	0.13	0.22	0.19	0.17	0.23	0.66	1.21	
carA2	38	40	36	43	42	44	44	47	51	33	42	11	-	0.12	0.13	0.10	0.15	0.12	0.12	0.20	0.20	0.21	0.13	0.10	0.13	0.16	0.11	0.14	0.59	1.30	
carA3	40	42	40	48	44	47	44	44	53	38	42	33	38	-	0.06	0.12	0.08	0.12	0.12	0.19	0.20	0.19	0.13	0.03	0.19	0.18	0.15	0.20	0.66	1.20	
carA4	38	31	33	43	36	38	36	38	44	36	33	33	33	11	9	4	-	0.12	0.08	0.10	0.24	0.19	0.20	0.07	0.06	0.19	0.18	0.14	0.20	0.69	1.26
carA5	29	38	33	39	38	38	36	42	49	27	36	36	33	11	9	9	-	0.09	0.09	0.17	0.17	0.16	0.16	0.09	0.09	0.17	0.16	0.12	0.18	0.62	1.22
carB	36	38	36	41	38	42	40	40	49	29	38	38	38	16	11	7	9	-	0.07	0.19	0.15	0.15	0.15	0.10	0.09	0.15	0.16	0.09	0.15	0.61	1.25
carC	33	40	36	41	40	42	42	42	51	31	33	33	33	18	11	11	7	9	7	-	0.24	0.19	0.19	0.10	0.09	0.15	0.16	0.09	0.15	0.61	1.25
fuln	40	44	44	43	40	49	42	49	51	40	44	44	44	20	13	18	20	16	18	22	-	0.25	0.25	0.20	0.21	0.17	0.15	0.17	0.74	1.31	
horn	29	36	38	43	33	38	36	36	40	29	33	33	33	18	13	16	13	11	11	13	20	-	0.05	0.14	0.15	0.23	0.21	0.20	0.23	0.62	1.36
litor	29	38	38	43	33	38	36	36	40	27	33	33	33	18	16	16	13	9	9	16	20	0	-	0.15	0.14	0.22	0.20	0.19	0.22	0.53	1.26
megaA5	32	34	34	41	34	39	34	39	45	30	36	36	36	14	9	9	5	2	7	7	16	7	7	-	0.10	0.14	0.11	0.08	0.14	0.58	1.37
megaB	38	42	38	45	42	44	44	42	51	33	40	40	40	11	9	2	7	9	9	9	18	9	11	7	-	0.16	0.15	0.14	0.17	0.62	1.22
virgA1	36	42	33	39	40	42	40	44	51	33	40	40	40	18	11	18	16	7	16	13	13	13	18	11	13	-	0.12	0.09	0.01	0.63	1.30
virgA2	27	33	29	34	31	33	31	38	40	24	31	31	31	16	11	11	13	9	13	9	11	11	11	7	9	4	-	0.13	0.14	0.56	1.29
virgA3	27	38	29	36	36	36	33	40	47	27	31	31	31	11	7	11	9	0	4	7	13	11	9	2	11	4	7	-	0.09	0.56	1.30
virgB	38	44	38	41	42	47	42	47	53	36	42	42	42	20	11	20	16	7	16	13	13	16	18	11	16	0	7	4	-	0.64	1.30
eger	32	45	30	44	36	36	36	34	39	34	39	34	39	48	43	48	48	41	45	43	52	39	39	40	43	45	39	48	-	1.18	
novo	62	62	62	57	58	56	56	62	62	60	60	60	60	69	71	67	69	71	69	69	73	69	69	70	69	71	71	71	71	73	66

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